Table 1 : Comparison of diagnostic methods for SMA

N° tube	SSCP[1]	Our méthod (radioactive) [3]					
		Probe 1 (exon 7)			Probe 2 (exon 8)		
	Exons [2]	PSL/mm²	R (%) [4]	Exon 7	PSL/mm²	R (%) [4]	Exon 8
Control (1)	ndel 7/ndel 8	42	0	ndel	22	0	ndel
Control (2)	ndel 7/ndel 8	41	0	ndel	23	0	ndel
Control (3)	ndel 7/ndel 8	43	0	ndel	22	0	ndel
Control (4)	ndel 7/ndel 8	41	0	ndel	21	0	ndel
Control (5)	ndel 7/ndel 8	42	0	ndel	23	0	ndel
SMA (6)	del 7/del 8	24	43	del	15	32	del
SMA (7)	del 7/del 8	14	67	del	08	64	del
SMA (8)	del 7/del 8	10	76	del	07	68	del
SMA (9)	del 7/del 8	26	38	del	06	73	del
SMA (10)	del 7/del 8	09	79	del	13	41	del
SMA (11)	del 7/del 8	27	36	del	12	45	del
SMA (12)	del 7/del 8	15	64	del	15	32	del
SMA (13)	del 7/del 8	13	69	del	14	36	del
SMA (14)	del 7/del 8	25	40	del	11	50	del
SMA (15)	del 7/del 8	20	52	del	09	59	del
SMA (16)	del 7/del 8	19	55	del	13	41	del
SMA (17)	del 7/del 8	12	71	del	14	36	del
SMA (18)	del 7/del 8	14	67	del	12	45	del

(1) single strand conformation polymorphism

(2) del : deleted ; ndel : non deleted

(3) The quantification of results obtained is performed by means of Bio-Imager and expressed as PSL/mm²

(4) R : difference = 1 - [(PSL/mm²Control - PSL/mm²SMA)/(PSL/mm²Control)]

The mean value of the control group is used for the calculation of R

Table 2 : Comparison of diagnostic methods for SMA

N° tube	SSCP (1)	Our method (ELISA)							
		Probe 1 (exon 7)			Probe 2 (exon 8)			Probe 3 (HUMEF1AB)	
	Exons (2)	Optical density	R(%)(3)	Exon 7	Optical density	R(%)(3)	Exon 8	Optical density	RT- PCR
Control (1)	ndel 7/ ndel 8	0.26	0	ndel	0.28	0	ndel	0.55	positive
Control (2)	ndel 7/ ndel 8	0.28	0	ndel	0.29	0	ndel	0.54	positive
Control (3)	ndel 7/ ndel 8	0.27	0	ndel	0.26	0	ndel	0.52	positive
Control (4)	ndel 7/ ndel 8	0.26	0	ndel	0.28	0	ndel	0.51	positive
Control (5)	ndel 7/ ndel 8	0.27	0	ndel	0.27	0	ndel	0.49	positive
SMA (6)	del 7/ del 8	0.16	41	del	0.13	54	del	0.51	positive
SMA (7)	del 7/ del 8	0.16	41	del	0.16	43	del	0.48	positive
SMA (8)	del 7/ del 8	0.11	59	del	0.12	57	del	0.53	positive
SMA (9)	del 7/ del 8	0.15	44	del	0.14	50	del	0.49	positive
SMA (10)	del 7/ del 8	0.19	30	del	0.16	43	del	0.5	positive
SMA (11)	del 7/ del 8	0.13	52	del	0.12	57	del	0.49	positive
SMA (12)	del 7/ del 8	0.14	48	del	0.13	54	del	0.48	positive
SMA (13)	del 7/ del 8	0.17	37	del	0.14	50	del	0.55	positive
SMA (14)	del 7/ del 8	0.12	55	del	0.15	46	del	0.52	positive
SMA (15)	del 7/ del 8	0.11	59	del	0.13	54	del	0.5	positive
SMA (16)	del 7/ del 8	0.13	52	del	0.15	46	del	0.51	positive
SMA (17)	del 7/ del 8	0.15	44	del	0.12	57	del	0.49	positive
SMA (18)	del 7/ del 8	0.16	41	del	0.16	43	del	0.5	positive

(1) single strand conformation polymorphism

(2) del : deleted ; ndel : non deleted

(3) R : difference = 1 - [(OD_{450}Control - OD_{450}SMA/OD_{450}Control)]

The mean value of the control group is used for the calculation of R